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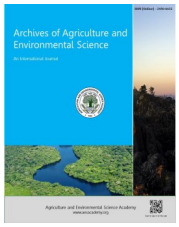

ORIGINAL RESEARCH ARTICLE

Genetic variation and morphological diversity in cowpea (*Vigna unguiculata* L. Walp)

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ABSTRACT

Cowpea is multipurpose pulse crop grown by poor and marginal farmers in arid zones of India. The extent of genetic diversity present in the cowpea accessions was studied for utilizing the most divergent parents for cowpea improvement programme. Genetic variability and genetic divergence was assessed in the 169 genotypes of cowpea using Mahalanobis D^2. High phenotypic and genotypic coefficient of variation, heritability and genetic advance were observed for days to 50 per cent flowering, number of branches per plant, number of pods per plant and seed yield per plant. The genotypes were grouped in to eight clusters, of which maximum intra cluster distance was exhibited by cluster VI and minimum by cluster II. The inter cluster distance was maximum between cluster II and IV. The genotypes from cluster II and IV, which have high and low cluster means for majority of the characters. The genetic advance estimates were medium to high (17.34% to 87.94%) for all the characters. seed yield contributed maximum towards the total diversity (48.05%), followed by days to 50 per cent flowering (21.08%), test weight (17.68 %), days to physiological maturity (3.58 %), plant height (3.49 %), pod length (1.69 %), number of clusters per plant (1.35 %), number of pods per plant (1.07 %), number of seeds per pod (0.75 %) lowest contribution was noted from number of branches (0.05 %) per plant. Therefore, genotypes from same regions are not recommended for hybridization because of close genetic background which was evident from the result showing genotypes belonging to same cluster.

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INTRODUCTION

Cowpea is one of the important arid legumes consumed both as green pod and dry seed in India. Like other pulse crops, cowpea fits well in mixed and multiple cropping systems. Cowpea is rich in nutritive value and it contains 24 per cent proteins, 60 per cent carbohydrates and 2 per cent fat besides being a good source of vitamins and phosphorus (Venkatesan *et al.,* 2003a; Chopra *et al.,* 2011; Srivastava *et al.,* 2016). At least 12.5 million hectares of cowpea are cultivated with an annual production over 3 million metric tonnes worldwide (Singh and Verma 2002). Development of new cultivar with early maturity, acceptable grain quality, resistant to some important diseases and pests has significantly increased the yield and cultivated area (Ehlers and Hall, 1997, Kenneth *et al.,* 2014). In order to achieve higher yield quantitative estimation of the genetic variability parameters along with the knowledge of genetic divergence is a pre requisite to the breeder to select genetically divergent parents with maximum potential to produce high heterotic combinations or chance of getting more segregation in their progenies. Keeping this view in mind 169 cowpea genotypes were subjected to variability parameters and genetic diversity analysis for further use in the cowpea improvement programme.

MATERIALS AND METHODS

In the present study, 169 cowpea genotypes that are maintained at the All India Co- ordinated research Project on Arid Legumes, University of Agricultural Sciences, Bangalore were used. These were from diverse origin representing the collections from different parts of India

and Nigeria. The crop was sown in Randomized Complete Block Design with two replications. Observations were recorded on five randomly selected plants in each genotype from each replication for ten quantitative characters, *viz.,* days to 50 per cent flowering, days to physiological maturity, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, test weight, seed yield per plant. The mean values of these observations were used to determine the range, mean, sum of squares and test of significance. The analysis of variance was calculated according to the method suggested by Panse and Sukhatme (1961). Phenotypic and genotypic coefficients of variation were worked out according to the method suggested by Burton and De Vane (1953) and Sivasubramanian and Menon (1973). Estimates of heritability and Genetic advance were computed by following the method of Robinson *et al.* (1949) and Johnson *et al.* (1955), respectively. Then data were subjected to multivariate statistic *i.e.* D^2 analysis (Mahalanobis, 1936) and the genotypes were grouped into different clusters following Tochers method (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance (ANOVA) revealed significant difference among the genotypes for all characters studied (Table 1) it indicates that wide range of variation exists among selected cowpea accessions for the study.

Genetic variability parameters: High estimates of PCV and GCV were observed for days to 50 per cent flowering, number of branches per plant, clusters per plant, pods per plant, pod length and seed yield per plant (Table 2), indicating greater scope for improvement of these characters through simple selection. These results are similar to the findings of Girish *et al.* (2006), Venkatesan *et al.* (2003a). Low PCV and GCV values were recorded for days to physiological maturity (Thiyagarajan, 1989), plant height, while moderate PCV and GCV values were reported for seeds per pod (Chauhan *et al.,* 2003; Kumari *et al.,* 2003), test weght (Neyaz and Bajpai, 2002; Venkatesan *et al.*, 2003b).

Heritability and genetic advance: The effectiveness of selection for any yield component depends not only on the amount of variability but also how much of it can be carried forward to future generations. In the present investigation, genetic advance estimates were medium to high (17.34% to 87.94%) for all the characters studied. This is mainly because of high GCV or h^2 or both. The characters like days to 50 per cent flowering, number of branches, number of pods per plant, pod length, seeds per pod and seed yield per plant exhibited high heritability along with high genetic advance indicating the importance of additive gene effects on these characters (Girish *et al.,* 2006; Venkatesan *et al.,* 2003b ; Kumari *et al.,* 2003). Days to physiological maturity recorded maximum heritability (97.84) compared to other traits. Days to 50 percent flowering exhibited maximum genetic advance (87.94%) compared to the other characters. Whereas number of clusters per plant and test weight expressed medium heritability coupled with high genetic advance. However, other reports indicating medium heritability and low genetic advance for the plant height (Omoigui *et al.,* 2006), primary branches per plant (Kumari *et al.,* 2000), seeds per pod (Selvam *et al.,* 2000), and also low heritability and low genetic advance for test weight (Selvam *et al.,* 2000; Singh and Verma 2002). High heritability estimate indicate less influence of environment on characters. Hence, direct selection can be followed to improve early maturing genotypes. High estimates of GA coupled with substantial amount of heritability indicate that selection for such characters would result in the improvement of characters in the desired direction.

Morphological diversity: The seed yield contributed maximum towards the total diversity (48.05%), followed by days to 50 per cent flowering (21.08%), test weight (17.68 %), days to physiological maturity (3.58 %), plant height (3.49 %), pod length (1.69 %), number of clusters per plant (1.35 %), number of pods per plant (1.07 %), number of seeds per pod (0.75 %) lowest contribution was from number of branches per plant (0.05 %) (Table 3). Rewale *et al*. (1996) reported maximum contribution towards the total diversity was by days to 50% flowering and maturity, number of pods per plant, pod length, 100-seed weight, and seed yield per plant. Similar results were also made by Backiyarani *et al.* (2000), Sulnathi *et al.* (2007). While Venkatesan, *et al*. (2003b) reported clusters per plant, pods per cluster, pods per plant and seed yield per plant had the maximum contribution towards total divergence. The 169 genotypes were grouped into eight clusters on the basis of Mahalanobis distance (Table 4). Cluster VI was the largest comprising of 51 genotypes followed by cluster VIII with 43 genotypes, cluster IV with 25 genotypes, cluster VII with 23 genotypes, cluster I with 16 genotypes, cluster V with 7 genotypes and cluster II and III had only two genotypes. Genotypes present in the more distanced clusters will serve as good sources of divergent genes which are very much required for breeding to exploit heterosis as reported by Gill *et al.* (1982).

The average intra and inter cluster distances are given in Table 5. Maximum intercluster distance was observed between the clusters II and IV indicating that the genotypes included in those clusters are highly divergent compared to genotypes in each clusters separately. The cluster mean values for each character in the clusters II and IV also indicated large differences between the cluster means for many characters. Minimum inter cluster distance observed between the cluster II and III and same was reflected in the cluster means for different characters showing small divergence between the clusters II and III.

Cluster VIII showing more D^2 distance with other clusters indicating that genotypes in the cluster VIII are more divergent from genotypes of other clusters. Intracluster D^2 value was small in the cluster II with only two genotypes whereas cluster VI has recorded maximum intracluster D^2 value indicating that, fifty one genotypes in the cluster VI were not closely related compared to the genotypes in the cluster II followed by the cluster V with seven genotypes. When we select the genotypes for hybridization it is desirable to select the genotypes from the clusters with maximum intercluster distance. The mean value for each

character across 8 clusters were calculated and good performing clusters with respect to overall performance was analyzed by giving rank to each cluster for individual character (Table 6). The lowest cluster mean for each character was given score '8' and highest one was given score '1' so that maximum total score that each cluster may secure would be 73 and minimum would be 12. In case of days to 50 per cent flowering early flowering type was given maximum ranking (8) and late flowering was given minimum rank(1). After analyzing 8 clusters based on rankings, cluster IV (score 12) found to have the genotypes with high overall performance. While, cluster II with low overall performance (score 73). It further indicates that genotypes from same regions are not recommended for hybridization because of close genetic background which was evident from the result showing genotypes belonging to same cluster.

Table 1. Analysis of variance (mean square) for ten quantitative characters in one hundred and sixty nine cowpea genotypes.

Sources of Variation	DF	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}
Replications	1	1.06	0.42	23.42	1.86	0.93	0.57	2.52	1.25	0.014	0.007
Genotypes	168	71.71**	104.80**	229.87**	2.50**	40.54**	131.14**	13.76**	6.94**	32.84**	64.58**
Error	168	0.62	1.08	3.18	0.23	5.56	16.73	2.05	1.87	0.46	1.85

*, ** - indicate significance at 5% and 1% level respectively; X_1 - Days 50 % flowering; X_2 - Days to physiological maturity; X_3 - Plant height (cm); X_4 - Number of branches per plant; X_5 - Number of clusters per plant; X_6 - Number of pods per plant; X_7 - Pod length (cm); X_8 - Number of seeds per pod; X_9 - Test weight (g); X_{10} - Seed yield per plant(g).

Table 2. Mean, range and Genetic variability parameters for ten characters in 169 cowpea genotypes.

S.N.	Characters	Mean± SE	Range	PCV (%)	GCV (%)	H^2 (%)	GA AS% Mean
1	Days to 50% flowering	50.89 ± 0.69	41.00-63.00	45.21	43.93	94.41	87.94
2	Days to physiological maturity	65.15 ± 1.40	59.00-90.00	9.25	9.15	97.84	18.64
3	Plant height(cm)	34.27 ± 4.31	8.57-57.68	8.93	8.67	94.23	17.34
4	Number of branches per plant	4.42 ± 0.90	2.33-8.64	31.40	28.77	83.96	54.31
5	Number of clusters per plant	12.84 ± 2.36	4.89-25.68	27.09	17.77	43.03	24.01
6	Number of pods per plant	20.45 ± 4.09	6.33-48.59	37.48	32.65	75.87	58.59
7	Pod length(cm)	14.60 ± 1.43	6.83-25.88	42.16	37.09	77.36	67.20
8	Number of seeds per pod	12.02 ± 1.37	8.12 -18.30	19.25	16.56	74.07	29.37
9	Test weight(g)	12.81 ± 0.68	5.70-28.65	17.46	13.23	57.47	20.67
10	Seed yield per plant(g)	12.74 ± 1.36	4.27-33.18	31.84	31.39	97.19	63.76

Table 3. Relative contribution of ten characters towards divergence in cowpea genotypes.

S.N.	Characters	Per cent contribution
1.	Days to 50% flowering	21.80
2.	Days to physiological maturity	3.58
3.	Plant height(cm)	3.49
4.	Number of branches per plant	0.05
5.	Number of clusters per plant	1.35
6.	Number of pods per plant	1.07
7.	Pod length(cm)	1.69
8.	Number of seeds per pod	0.75
9.	Test weight(g)	17.68
10.	Seed yield per plant(g)	48.05

Table 4. Clustering pattern of 169 cowpea genotypes based on D^2 analysis.

Clusters	Number of genotypes	Genotype
I	16	4C3, 198355(45), 201095(52), 202705(54), 202709(56), 202804(83), 202827(92), 202827(93), 202854(97), 257422(7), 27749(25), IC 402101, 97767(10), C – 16, C - 24 – 1, C – 33
II	2	IC 202290, IC 402099
III	2	NBC 10, NBC 18
IV	25	C 131 + C 132, C 152, C 304, C 325, C 347, C 388– 2, C 457, C 503, C 517, C 710, C 720, IC 202777, IC 202789(73), KBC 2, KM 5, TVX 944, V 240, CP 58, CP 66, CP 82, V 578, V 578–17, V 578–27, V 578–30, V 604 -7-24–2
V	7	C 787, C 795 – 1, C 1061, C 1071, CP10, CP 15, CP 55
VI	51	CP 98, CP 101, CP 102, C-PD–15, CPD 15, CPD 31, CPD 35, EC 170578-1–1, EC 170584, EC 170584-1–1, EC 170584 -1-1-13, EC 170584B9, EC 170604, EC 390287, EC 394779, EC 394839, EC 458402, EC 458411, EC 458418, EC 458425, EC 458430, EC 458438, EC 458440, EC 458441, EC 458442, EC 458453, EC 458469, EC 458472, EC 458473, EC 458480, EC 458483, EC 458485, EC 458489, EC 458497, EC 458506, EC 458511, EC 458513, EC 472217, EC 472250, EC 472252, EC 472257, EC 488475, FTC 27, GC 3, IC 1071, IC 4506, IC 49586, IC 202711(58), IC 402162
VII	23	IC 202781, IC 202789(73), IC 202797(78), IC 202825(89), IC 202867(99), IC 249588, IC 249593, IC 253251, IC 330996, IC 402098, IC 402106, IC 402125, IC 402166, IC 402174, IC 402180, IC 198326(34), IC 1983299(36), IC 19832946, IC 20285164, IC 2591054, IT 38956-1, NBC 34, NBC 35
VIII	43	IT 9715499–38, KBC 1, TC 201, NBC 6, NBC 7, NBC 11, NBC 12, NBC 13, NBC 14, NBC 15, NBC 16, NBC 17, NBC 18, NBC 19, NBC 20, NBC 21, NBC 22, NBC 25, NBC 27, NBC 28, NBC 29, NBC 32, NBC 33, NBC 36, NBC 38, NBC 39, NBC 40, NBC 41, NBC 42, NBC 43, NBC 44, NBC 45, NBC 47, NBC 48, NBC 50, NBC 51, NBC 52, NBC 53, TC 99– 1, TOME 774, V 130, V 152 , V 585 , V 585–1

Table 5. Average intra and inter cluster D^2 values.

Cluster	I	II	III	IV	V	VI	VII	VIII
I	310.559	376.10	349.501	652.226	361.398	351.442	367.414	378.59
II		140.65	64.586	1158.944	168.244	478.984	262.536	294.609
III			263.41	1070.299	166.676	429.714	234.357	266.689
IV				318.961	1026.734	582.587	888.724	817.678
V					218.362	432.347	282.136	331.791
VI						366.604	419.685	409.384
VII							336.7	361.543
VIII								358.517

Diagonal values indicate intra cluster distances; Above diagonal values indicate inter cluster distances.

Table 6. The mean values of clusters for quantitative parameters in cowpea genotypes.

Clusters	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	Over all Score	Rank
I	52.83 (3)	69.42 (3)	36.88 (3)	4.82 (3)	13.15 (5)	20.87 (5)	12.91 (8)	12.82 (3)	11.75 (6)	10.11 (5)	41	3
II	48.00 (5)	59.00 (7)	20.13 (8)	3.90 (7)	8.45 (7)	10.65 (8)	14.82 (4)	11.83 (5)	11.45 (7)	8.77 (8)	73	8
III	47.00 (6)	58.00 (8)	27.67 (7)	4.50 (5)	21.84 (1)	32.17 (2)	13.61 (7)	11.50 (8)	10.90 (8)	11.63 (4)	61	6
IV	61.69 (1)	78.65 (1)	46.76 (1)	5.33 (1)	18.66 (2)	37.60 (1)	17.11 (1)	16.73 (1)	17.91 (1)	19.34 (1)	12	1
V	46.33 (8)	62.22 (6)	30.64 (6)	3.40 (8)	8.11 (8)	12.25 (7)	13.76 (6)	11.63 (6)	12.11 (5)	9.66 (7)	69	7
VI	53.20 (2)	69.80 (2)	39.43 (2)	4.79 (4)	13.61 (4)	22.20 (4)	15.07 (3)	12.90 (2)	13.51 (2)	14.90 (2)	31	2
VII	50.46 (4)	62.80 (5)	34.43 (4)	4.15 (6)	12.35 (6)	19.77 (6)	15.64 (2)	12.73 (4)	12.53 (4)	10.67 (6)	53	5
VIII	49.30 (4)	64.80 (4)	31.98 (5)	4.87 (2)	13.86 (3)	22.50 (3)	14.47 (5)	11.55 (7)	13.17 (3)	14.66 (3)	45	4

Figures in parenthesis, indicate the ranks based on cluster mean, highest (1) to lowest (8) except days to 50% flowering. Overall score is the summation of rank number for 10 characters.

Conclusions

Diverse genotypes selected from different clusters with extreme characters will be used as parents for hybridization and development of mapping population for future plant breeding for the development of superior varieties of cowpea.

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